This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problems Mailbox.

EXHIBIT 2

Confidential Poster Presentation

by

William H. Barber

Submitted with the 37 CFR § 1.131 Declaration of William H. Barber, in the RCE filed in Application Serial No. 09/578,631

[redacted]

Colorado Poster Session
August 15, 1997

Abstract Titles

TNFα/sTNFR1

1. [redacted]
2. [redacted]
3. [redacted]
4. [redacted]
5. [redacted]
6. [redacted]

[redacted]

44.

45.

46.

Drug Metabolism/Analytical Chemistry

47.

48.

49.

50.

51. Open Access ESI/Mass Spectrometry: A Walk-up MS Service
Bill Barber, Xiaobing Xiang and Eric Watson

52.

53.

54.

High Speed Synthesis

55.

56.

PURPOSE.

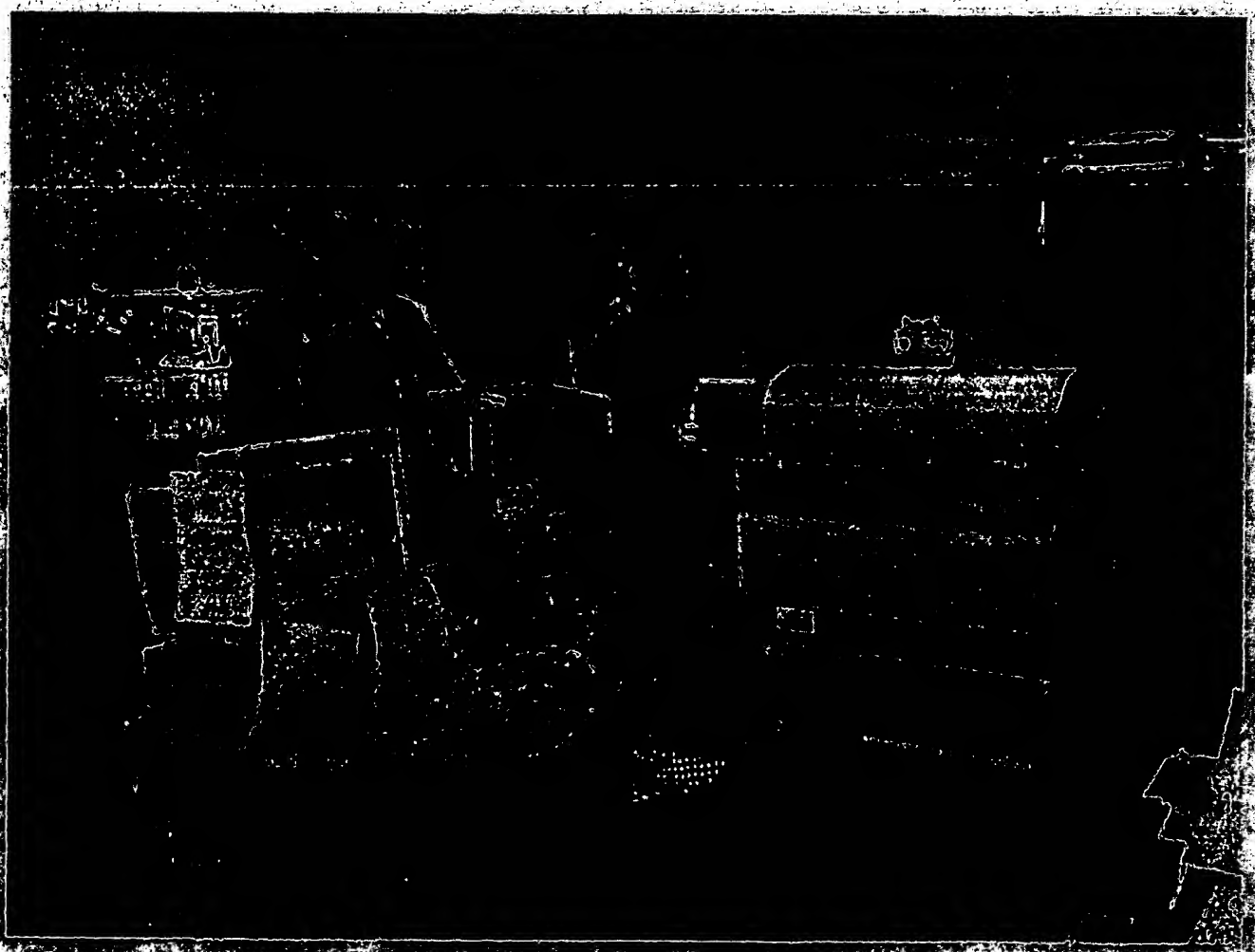
METHOD:

Buffers:

A key element in automated, open access analysis of a wide variety of compound classes has been the development of a single standardized MS system. A universal mobile phase had to be developed that would couple with electrospray ionization to produce a mild ionizing atmosphere with negligible fragmentation. It has recently been determined that a water / acetonitrile / 0.03% ammonium hydroxide solvent system is suitable for determining molecular weights for well over 98% of compound types generated on site.

Equipment.

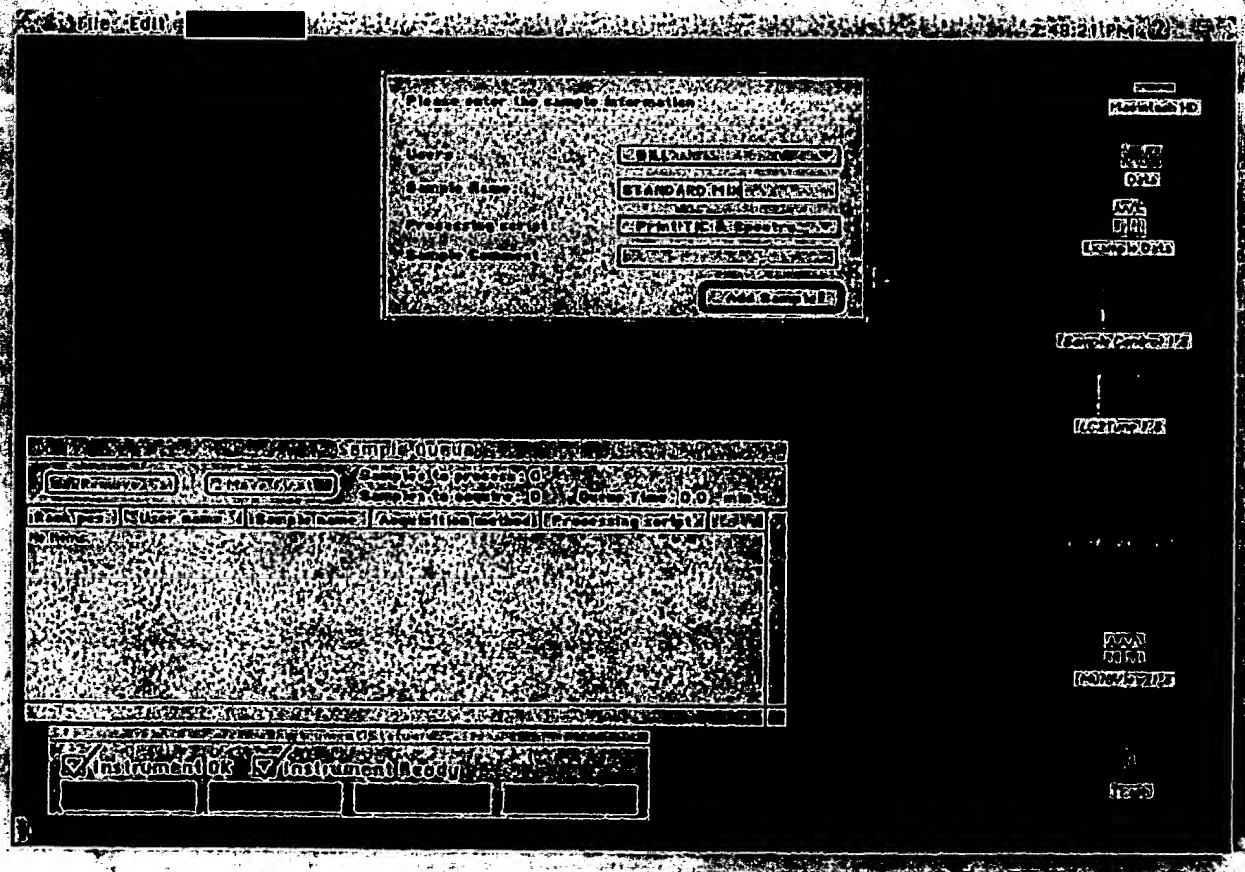
Hardware and software systems manufactured by Perkin Elmer / Sciex have been modified for our medicinal chemistry department to allow for minimal analyst input and maximum reliability. To simplify user access, a multifunctional user interface controls all the system components.



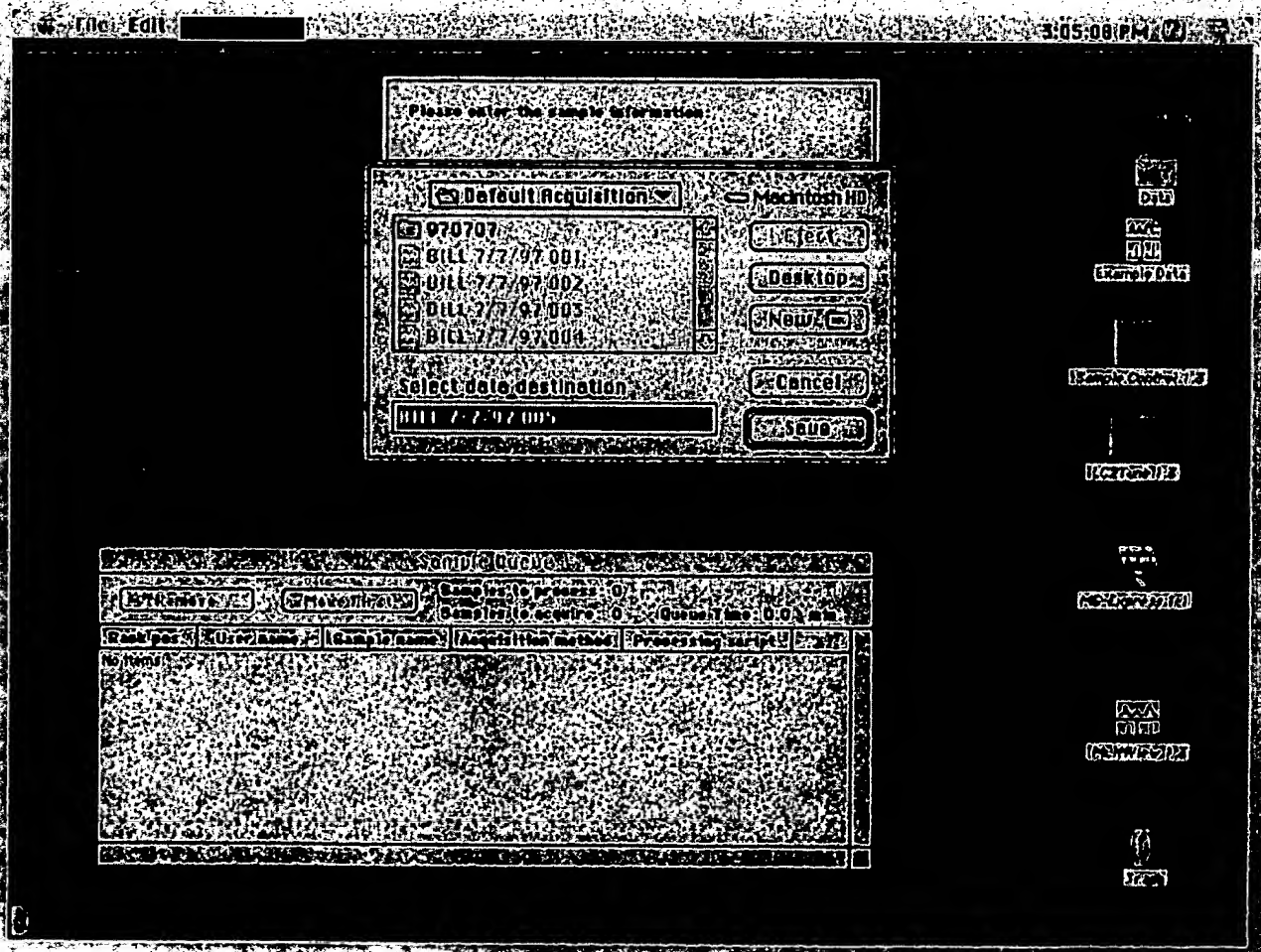
The Open Access System is vigilantly maintained by the system administrators

Software

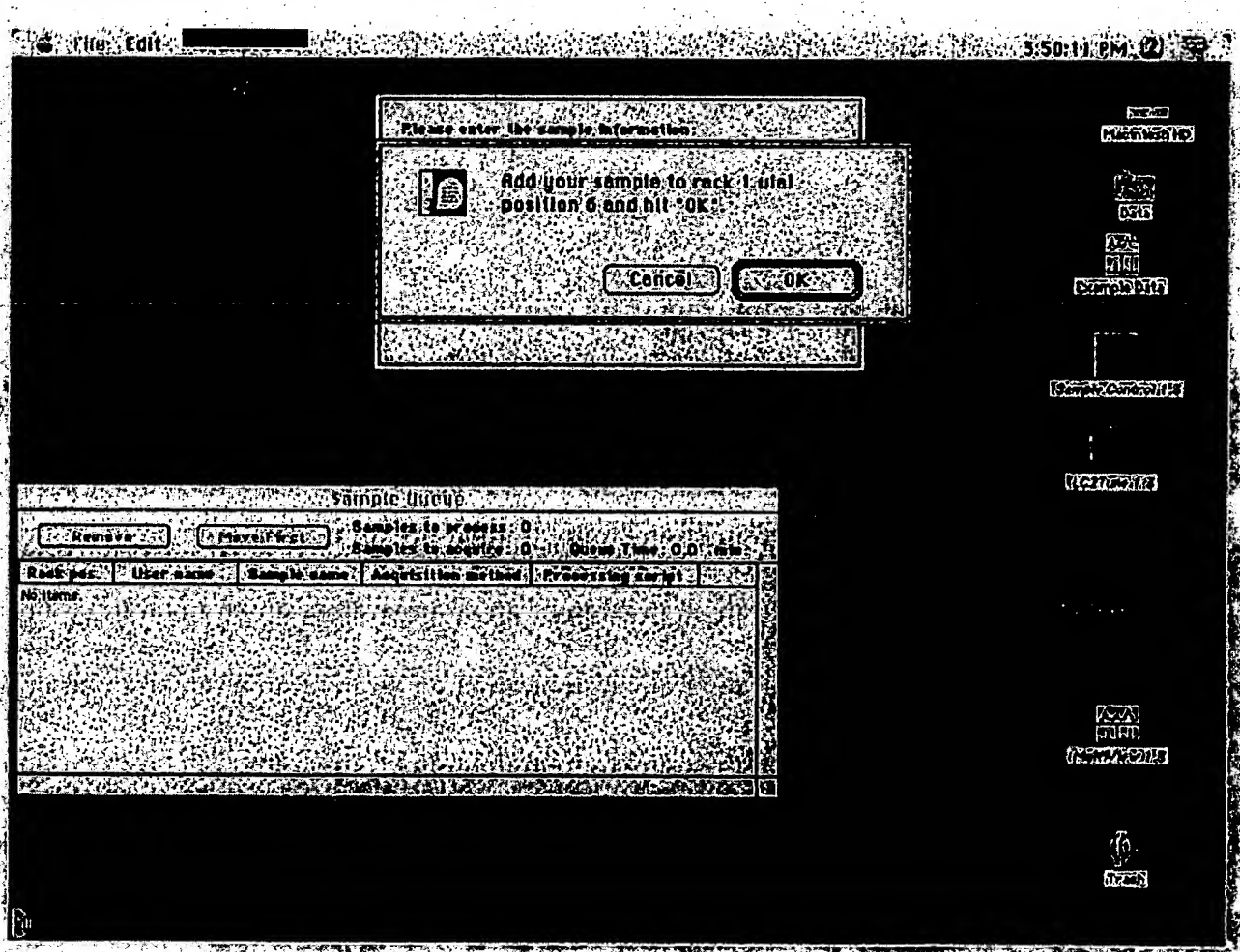
[redacted] is designed to be flexible enough for an administrator to select from a variety of input parameters to meet the needs of the users. For molecular ion determination in the synthetic chemistry labs, [redacted] has been set up to have the fewest possible input requirements. The user name is selected from a pull down menu that has been pre loaded by the system administrator. Sample information, such as a notebook number, can be entered up to 32 characters. The processing script, "Print TIC & Spectrum", is selected from the pull down menu. Sample comments are optional and will also appear on the printout. The "add sample" button directs the user to the file selection window.



All samples **must** be filed within the "Default Acquisition" folder. If a user is entering multiple samples, the default label will be automatically held for 30 seconds with the user name, date, and incremented run number (ex. Bill 7/7/97 001). Clicking on the "save" button enters the sample into the queue and the system notifies the user into which autosampler position the vial is to be placed.

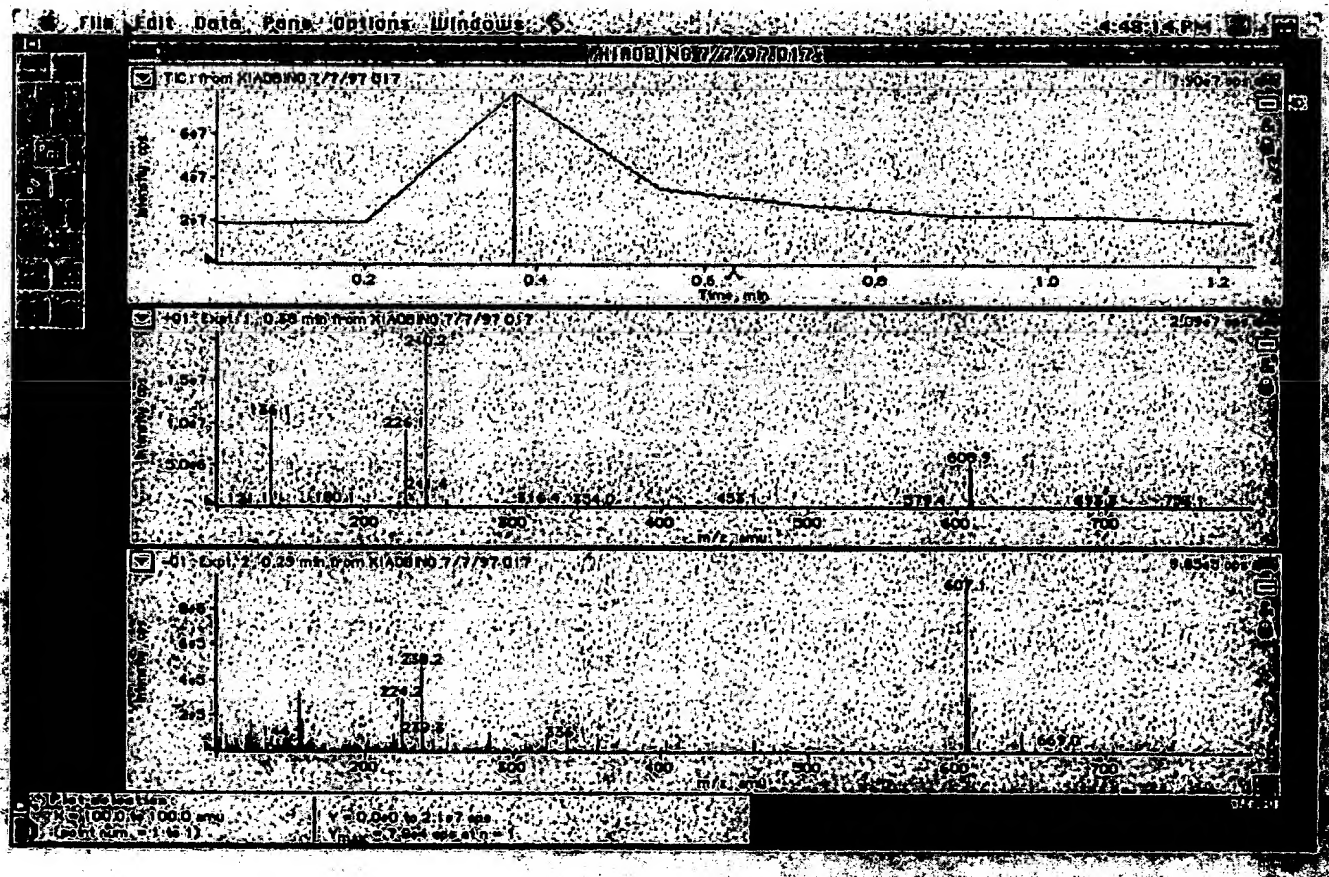


Once the vial is in the requested position the user clicks the "OK" button and the mass spec takes over.



RESULTS FORMAT

At the end of the run, a post-run "Apple Script" is automatically activated that selects the largest peak in the total ion chromatograph (TIC), generates spectra in both positive and negative modes, and spools a one page print out that contains the TIC, and the two spectra. Results appear on the printout only. No on-screen information will be available. Below is an example of a single run of our standard mix which contains 4 compounds with individual molecular weights as follows: 4-amino benzamidine-135, Terbutaline-225, Salbutamol-239, and Reserpine-608.



1. The total Ion Chromatograph (TIC) is shown in the first panel.
2. The positive ion spectra in the second panel shows the $(M+H)^+$ ions of the four standards.
3. The negative ion spectra is shown in the last panel.

SPEED AND UTILITY

Though the [redacted] software is designed to process batches as well as individual samples, the key to the utility of an open access system is its availability to the maximum number of users throughout the work day. To maintain access, individual and small batch runs are encouraged.

Organic chemists are now independently carrying out their own automated MS analysis with great success and total run times around two and a half minutes. Both positive and negative ionization modes are performed within the same run through 6 second switching intervals.

CONCLUSIONS

For this system, samples are entered individually. Additional samples can be entered into the system while others are running. This builds a sample queue that will run until complete. Individual runs take 2 minutes and 45 seconds from "Go" to "print out", however a batch of queued samples will be completed faster as multi-tasking takes place during printing. No data manipulation is required or is possible and print outs are available on the "MS API" printer located next to the API III. Logging in samples at the lab entrance is no longer necessary and all data files will be discarded at the end of each week. To maintain system reliability, samples should be in Perkin Elmer approved autosampler vials and dissolved in the standard ms buffer; H_2O : MeOH : ACN (1:1:1).